A-U AUAAACUAAGGAAUaucuaug d-G C-G G-C -20 . uaauauau CAAG

SEQ. I.D. NO. 345

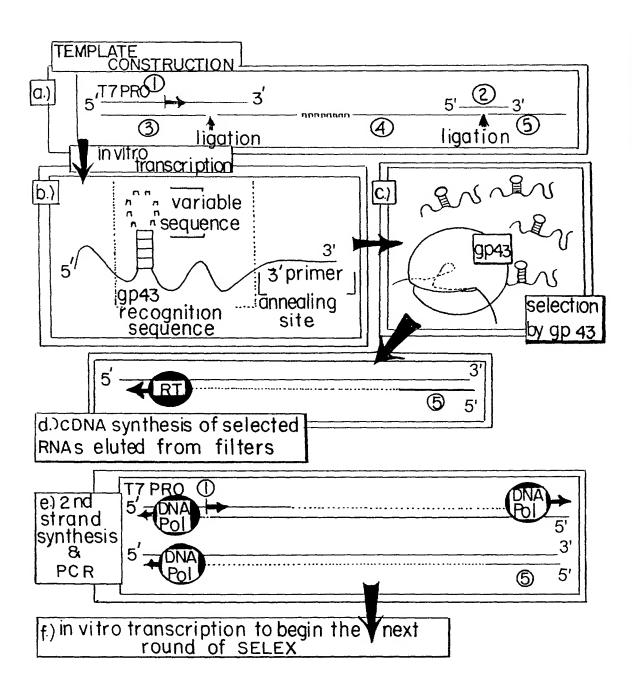
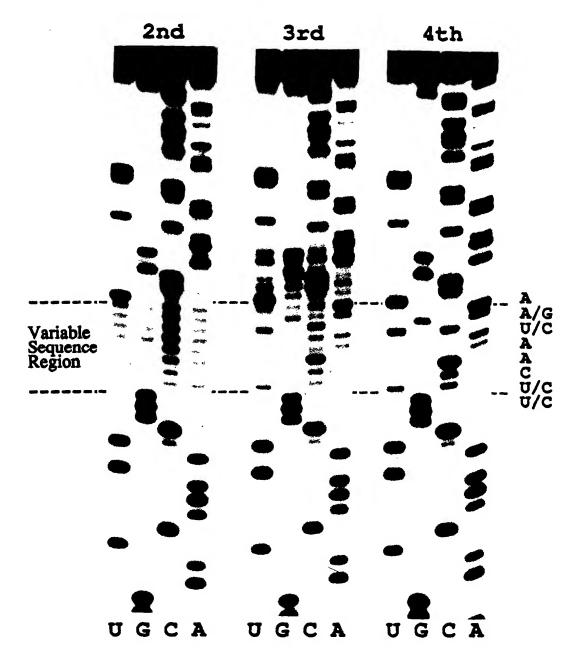


FIG.2

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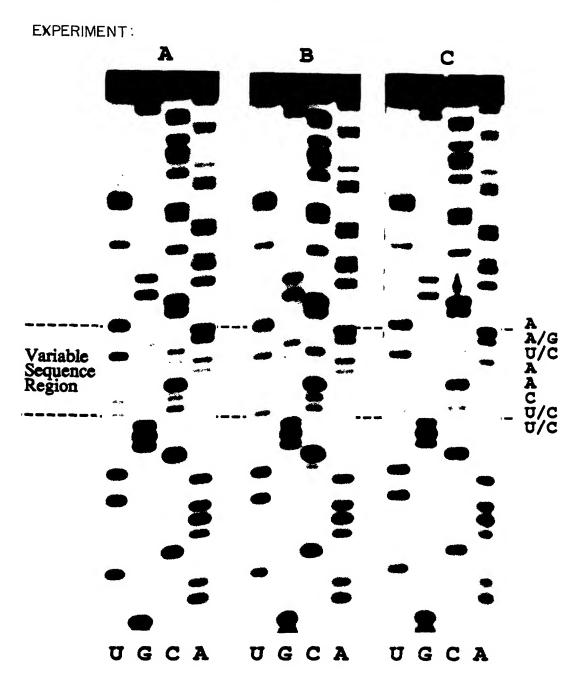
FIG.3

SELECTION CYCLE:

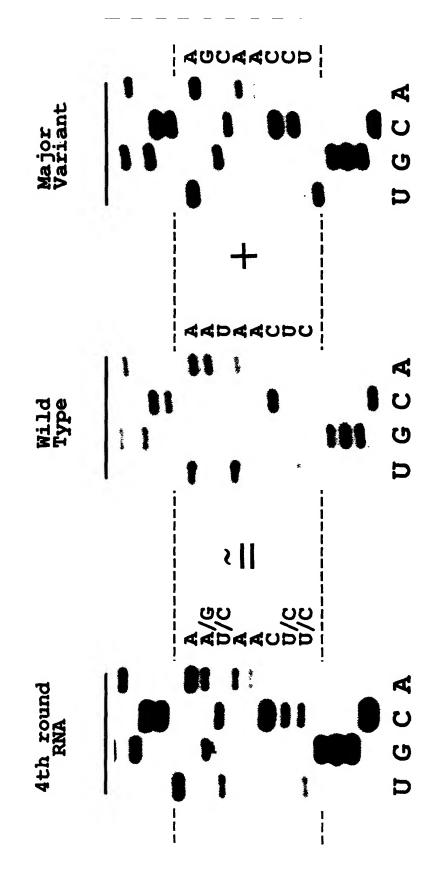


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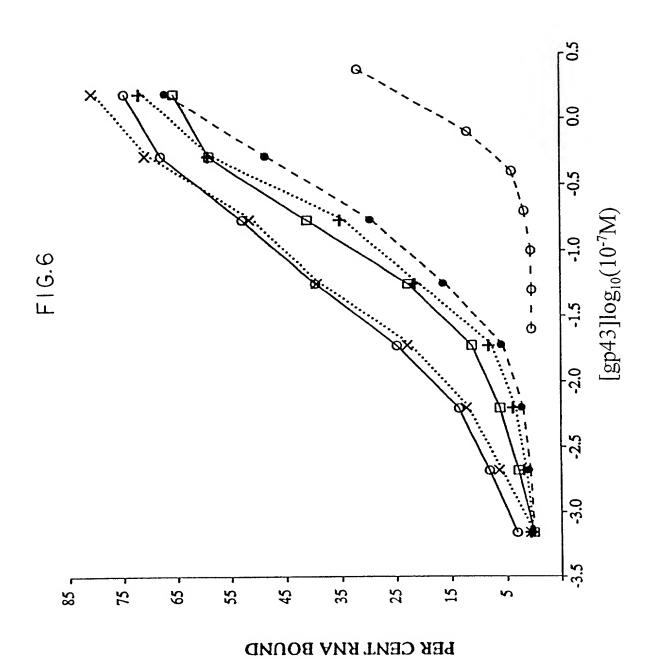
FIG.4

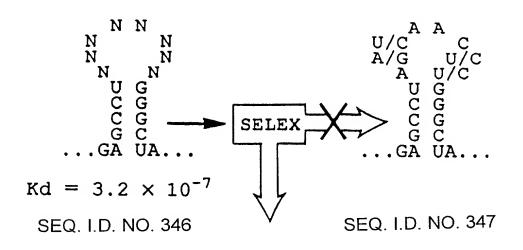


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F16.5





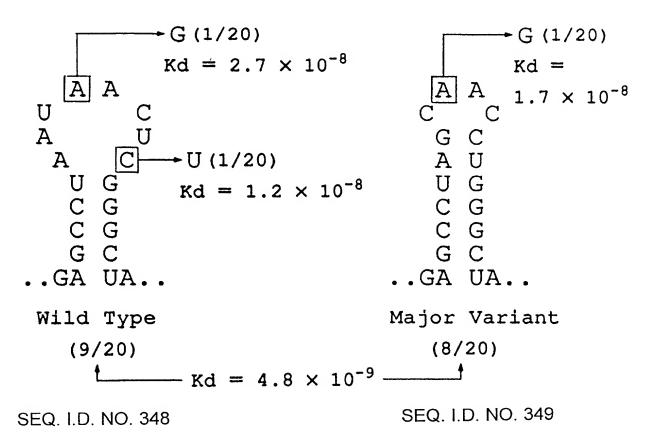


FIG.7

VARIABLE TEMPLATE SYNTHESIS USING TERMINAL TRANSFERASE 5'PRIMER (OR PRIMARY LIGAND SEQUENCE) 3 PRIMER TAILING WITH TERMINAL TRANSFERASE USING RANDOM NUCLEOTIDES **dNTPs** HOMOPOLYMER TAILING OF LENGTHENED 5' PRIMER & 3' PRIMER. **dCTP** GGGGGG-3' PRIMER ANNEALLING & FILLIN 5

FIG.8

DNA

"WALKING" BY EXTENDING THE PRIMARY LIGAND.

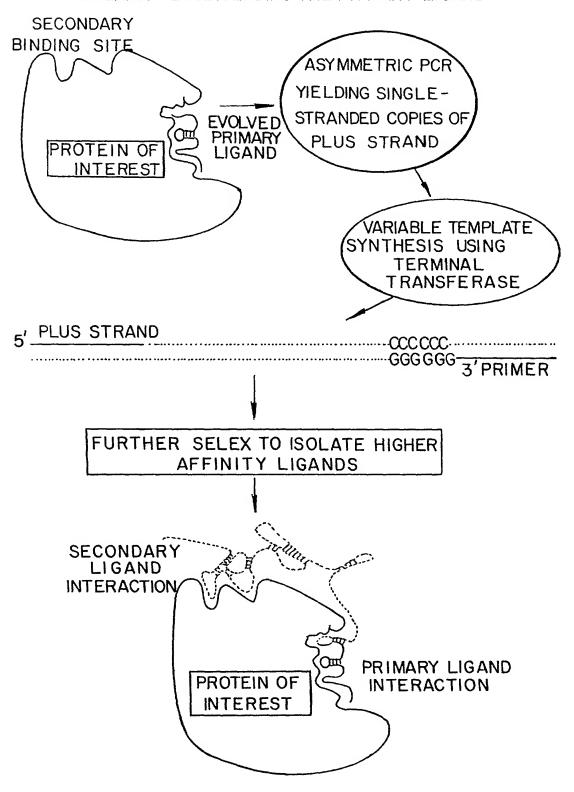


FIG.9

and the continue of the contin

ANCHORING OF BRIDGING OLIGONUCLEOTIDE & SECONDARY LIGAND EVOLUTION.

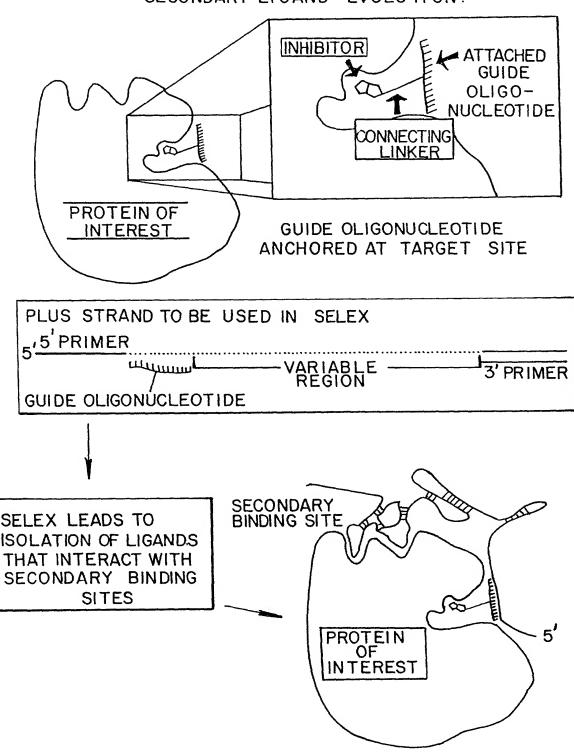


FIG.10

SECONDARY LIGAND-DIRECTED PRIMARY LIGAND EVOLUTION. DOUBLE-STRANDED TEMPLATE IS RESTRICT-ION ENDONUCLEASED AT GUIDE ANNEALING SITE PROTEIN OF CUT INTEREST INSERTION OF VARIABLE SEQUENCE AT GUIDE SITE FURTHER SELEX TO EVOLVE LIGANDS TO PRIMARY TARGET DOMAIN **SECONDARY** LIGAND INTERACTION PRIMARY LIGAND INTERACTION **PROTEIN** OF **INTEREST**

FIG.11

AND THE REPORT OF THE PERSON O

3'-gttagttc

F16.12B taatacgactcactatagggagcatcagacttttaatctgacaatcaag-. 3'-attatgctgagtgatatccctcgtagtctgaaaattagact-5' ligation SEQ. I.D. NO. 350 SEQ. I.D. NO. 351 promoter T7

5'-gggagcaucagacuuuuaaucugacaaucaag[32n]aucuaugaaagaauu

in vitro transcript

F16.12A

FIG. 12 B

3'-cttaaaatatagagataactttgcctaggcc-5' 5'-atctatgaaagaattttatatctc-3'

SEQ. I.D. NO. 352

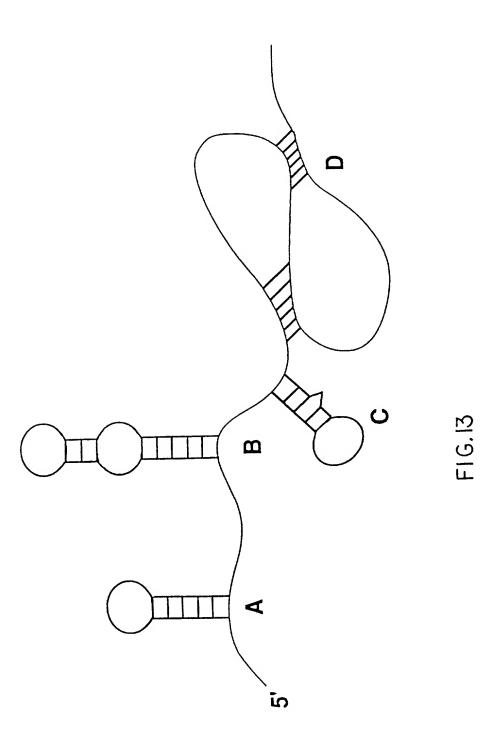
ligation

32n..tagatacttt-5'

SEQ. I.D. NO. 353

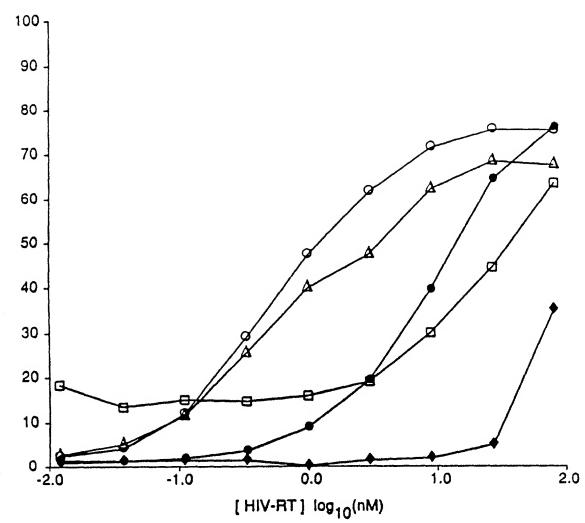
unauaucucuaungaaacggauccgg-3' SEQ. I.D. NO. 354

F16.12B









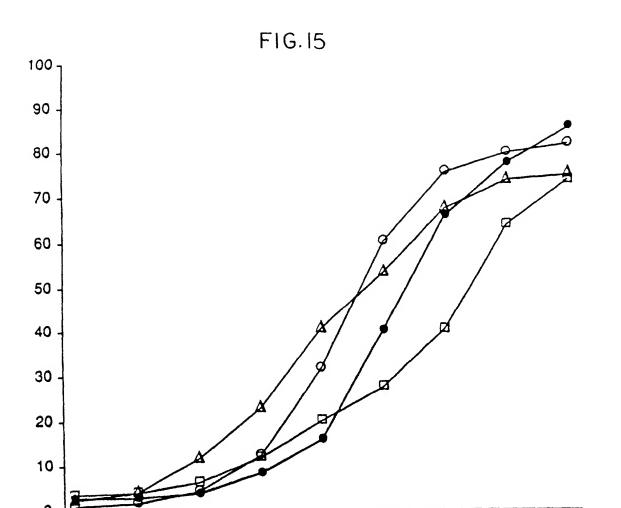
- Δ 1.1 ucaagaauuccguuuucagucgggaaaaacugaaca aucu (13)
- O 1.3 UCAGAAUAUCUUCCGAAGCCGAACCGGAAACCGGCAUCU (1)
- ☐ 1.4 ucaagGGCAUCUGGGAGGGUAAGGGUAAGGUUGUCGGaucu (4)

 \triangle 1.1 = SEQ. I.D. NO. 355

● 1.3 = SEQ. I.D. NO. 357

O 1.3 = SEQ. I.D. NO. 356

☐ 1.4 = SEQ. I.D. NO. 358



0.0

[HIV-RT] log₁₀(nM)

-1.0

☐ 2.2b = SEQ. I.D. NO. 360

-2.0

2.0

1.0

AND REPORTED THE PROPERTY OF T

 \triangle 1.1 = SEQ. I.D. NO. 362

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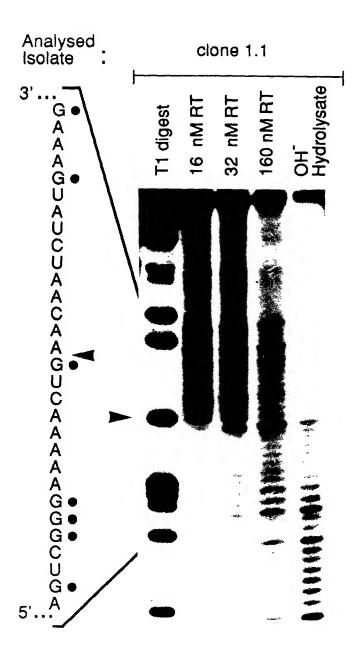


FIG. 16 A

SEQ. I.D. NO. 363

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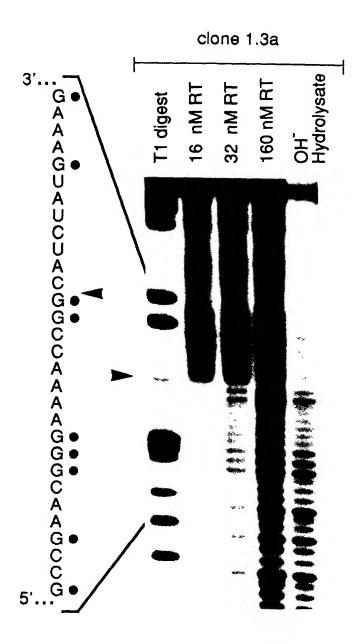
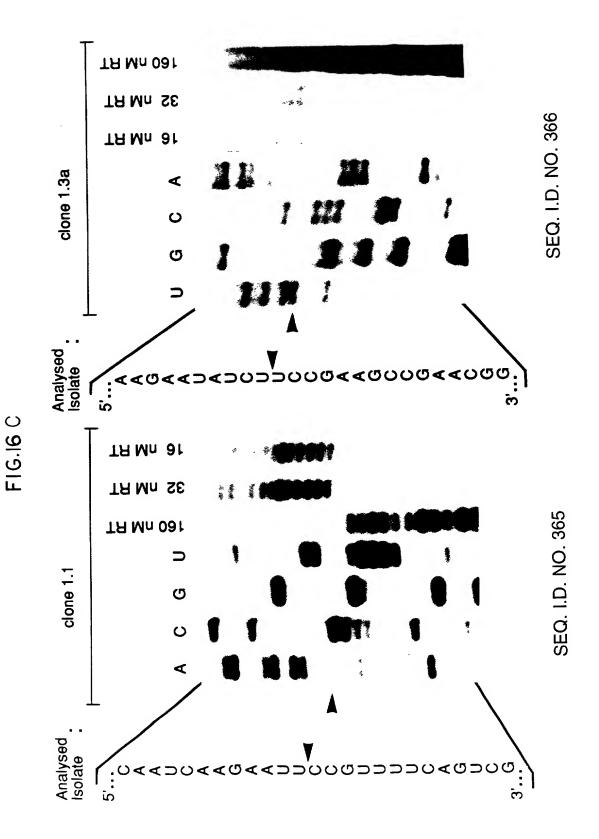


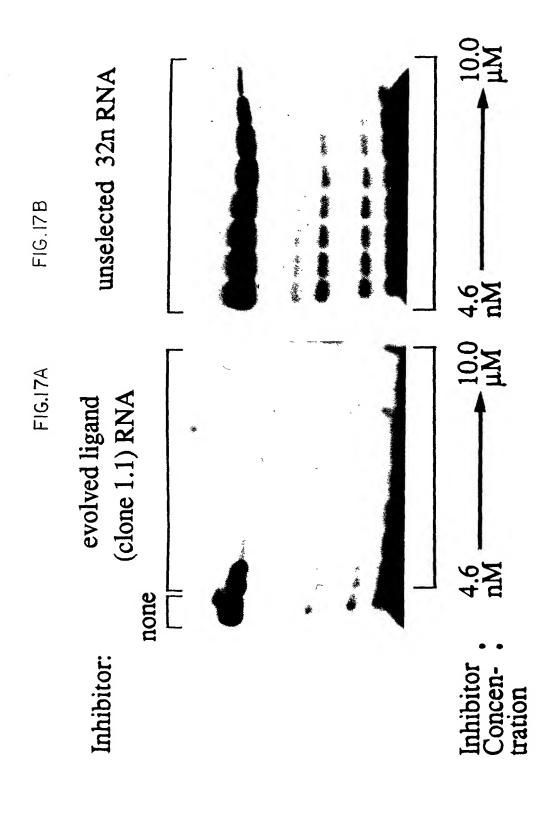
FIG.16B

SEQ. I.D. NO. 364

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Inventor: Gold et al
Express Mail No. EL652339952US

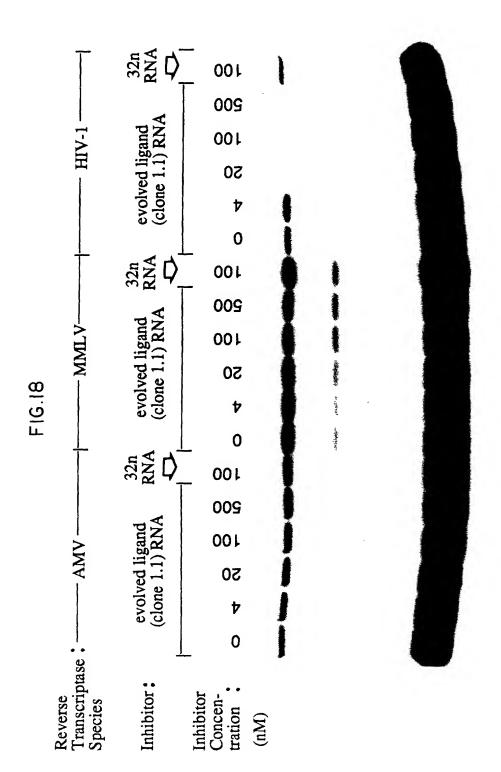
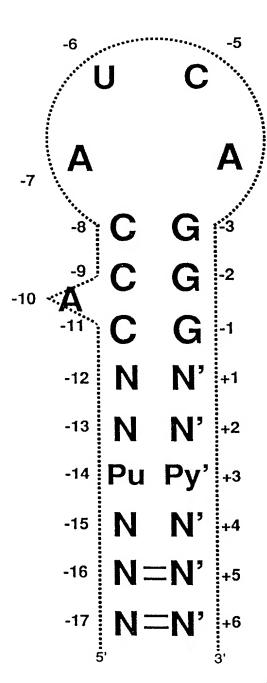


FIG.19B



		Α	С	G	U	
[-	4	36	0	0	0	
-	5	0	36	0	0	
-	6	4	3	1	28	
-	7	36	0	0	0	
-1	10	36	0	0	0	

	AU	CG	UA	GC	UG	GU	Bulge	END
-8/-3	0	24	0	12	0	0	0	0
-9/-2	0	25	0	10	1	0	36	0
-11/-1	0	24	2	10	0	0		1
-12/+1	8	1	8	10	7	1	0	
-13/+2	6	5	8	9	3	1	3	3
-14/+3	9	0	4	10	2	3	3	4
-15/+4	4	0	9	6	0	1	6	8
-16/+5	10	1	2	1	1	3	0	2
-17/+6	0	4	6	1	4	2	1	1

FIG.19C

FIG.19A

SEQ. I.D. NO. 367



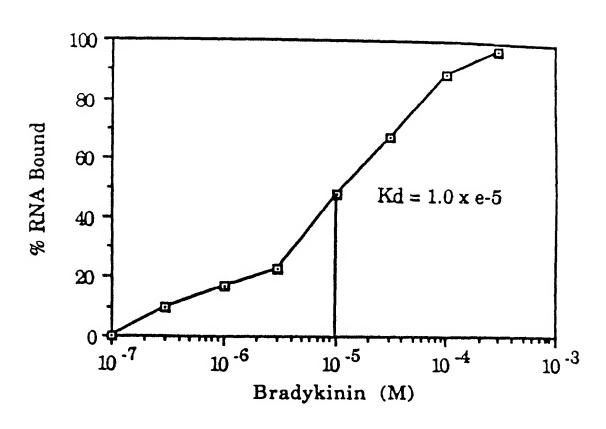
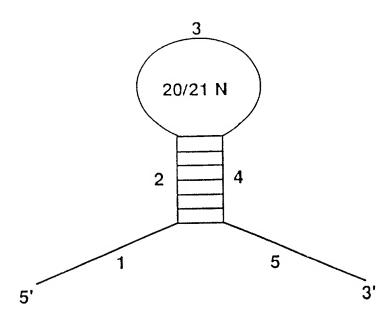


FIG.21A



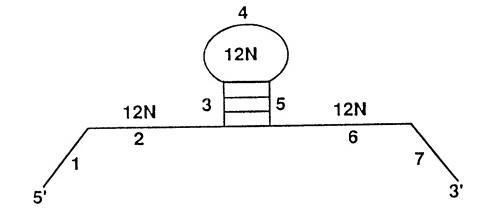
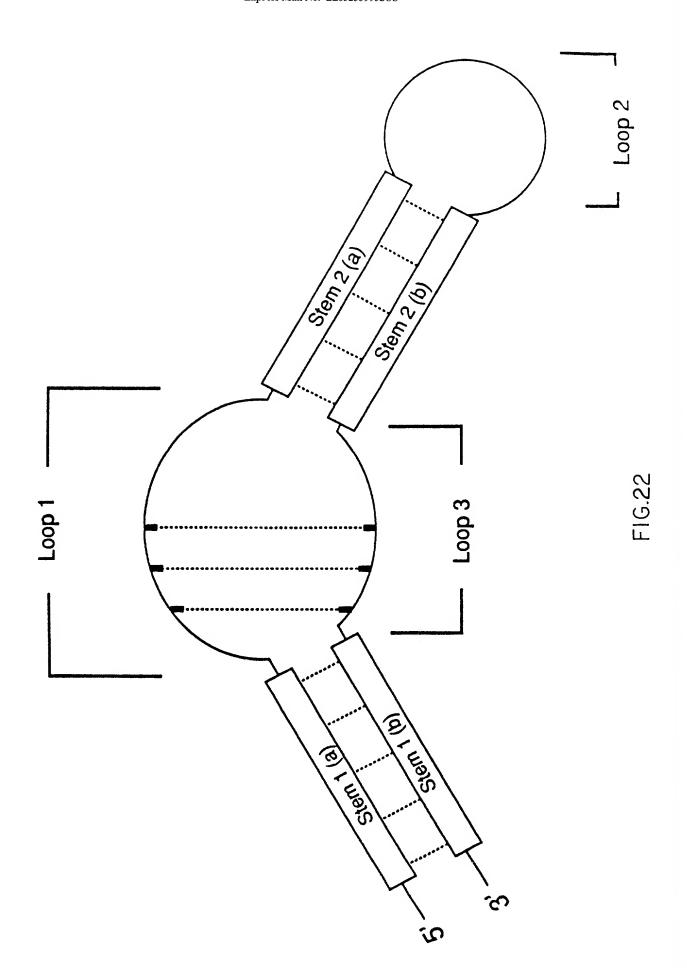


FIG. 21B

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KODWYSS JOHSOK

Motif I (6a)

UUGAGAAA --CUCA-G 5'...gGGUGCA 3'...ucuaUGU

Motif III (9a)

Motif II (1c)

ugaa-3' GCUU-5' CC UUGaucua-

SEQ. I.D. NO. 369

SEQ. I.D. NO. 368

UAG

-ACA-G

GUCG CAGC

5'...AGAUG 3'...ucuAC

AAGAUA

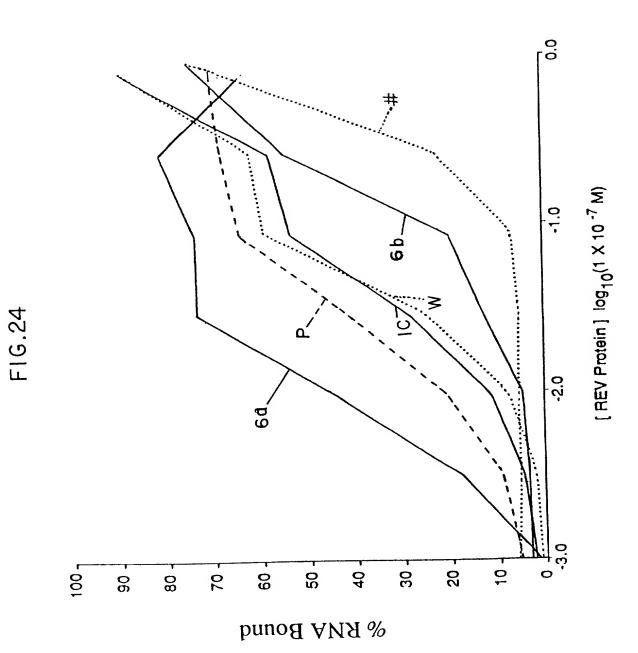
WT (Motif II-like Domain)

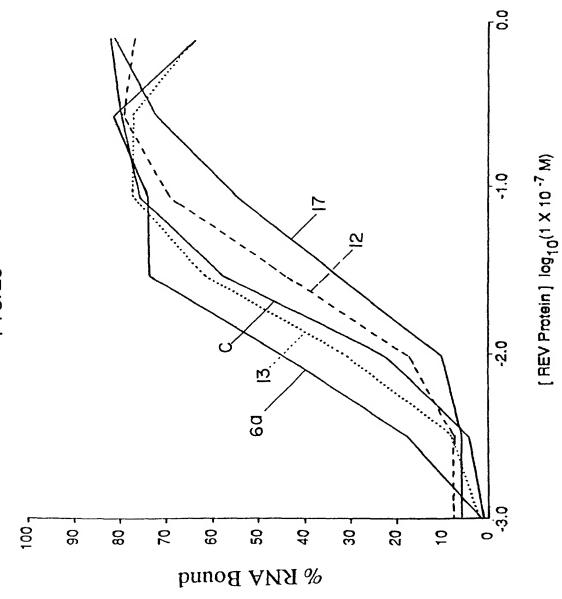
D ACGGUA
A GACGCUG | | CA...
CUGCGAC | | GU... 9-909-

SEQ. I.D. NO. 370

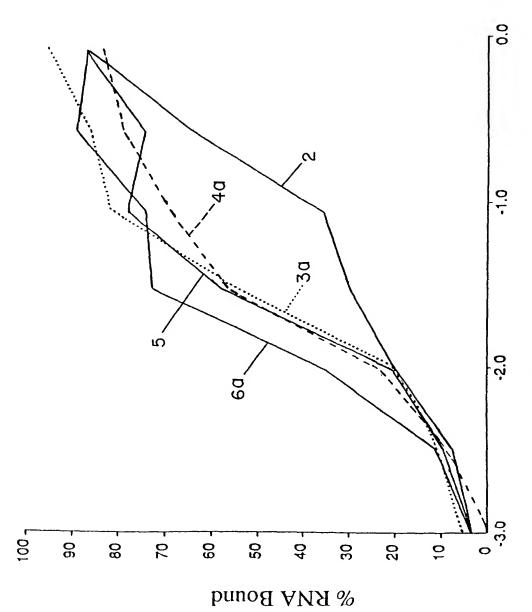
F1G. 23

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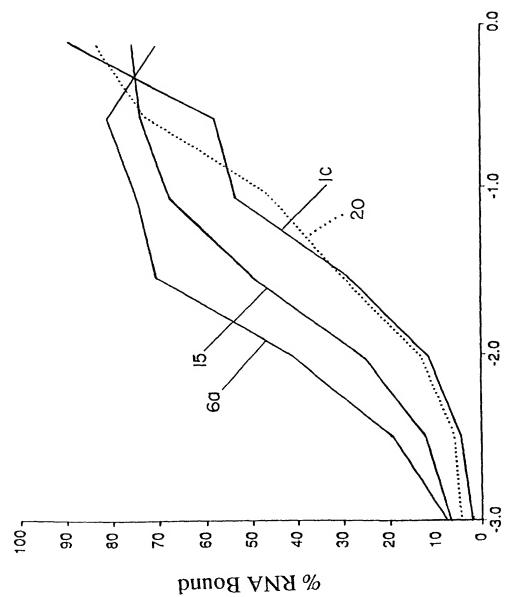




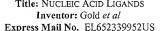


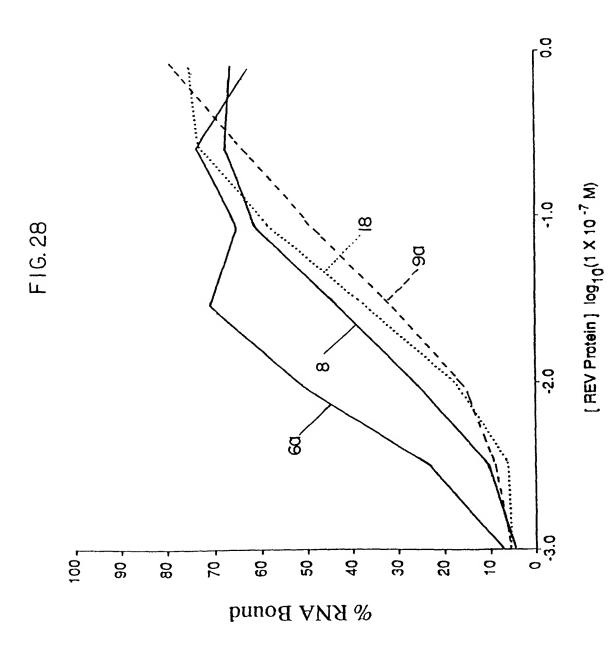
[REV Protein] $log_{10}(1 \times 10^{-7} M)$

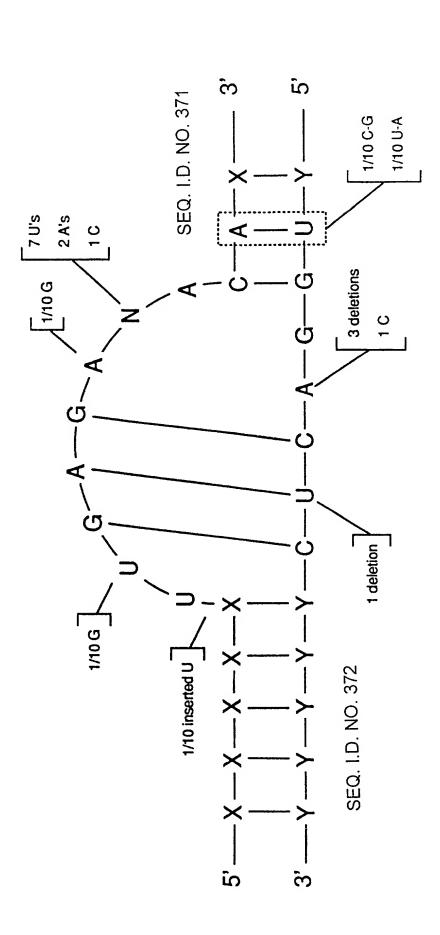




[REV Protein] $\log_{10}(1 \times 10^{-7} \,\mathrm{M})$







-16.29

